

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number:

10/722,045

Source:

EFW

Date Processed by STIC:

11-19-04

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IFWO

RAW SEQUENCE LISTING

DATE: 11/19/2004

PATENT APPLICATION: US/10/722,045

TIME: 16:50:33

Input Set : D:\7682108999.txt

Output Set: N:\CRF4\11192004\J722045.raw

3 <110> APPLICANT: DeJong, Jan
 4 Fouchier, Ronaldus
 5 Van Den Hoogen, Bernadetta
 6 Osterhaus, Albertus
 7 Groen, Jan
 9 <120> TITLE OF INVENTION: Virus causing respiratory tract illness in susceptible
 mammals
 11 <130> FILE REFERENCE: 7862-108-999
 13 <140> CURRENT APPLICATION NUMBER: 10/722,045
 14 <141> CURRENT FILING DATE: 2003-11-25
 16 <150> PRIOR APPLICATION NUMBER: 10/466,811
 17 <151> PRIOR FILING DATE: 2003-07-18
 19 <150> PRIOR APPLICATION NUMBER: PCT/NL02/00040
 20 <151> PRIOR FILING DATE: 2002-01-18
 22 <150> PRIOR APPLICATION NUMBER: EP01200213.5
 23 <151> PRIOR FILING DATE: 2001-01-19
 25 <150> PRIOR APPLICATION NUMBER: EP01203985.5
 26 <151> PRIOR FILING DATE: 2001-10-18
 28 <160> NUMBER OF SEQ ID NOS: 165
 30 <170> SOFTWARE: PatentIn version 3.2
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 394
 34 <212> TYPE: PRT
 35 <213> ORGANISM: Human metapneumovirus 00-1
 37 <400> SEQUENCE: 1
 39 Met Ser Leu Gln Gly Ile His Leu Ser Asp Leu Ser Tyr Lys His Ala
 40 1 5 10 15
 43 Ile Leu Lys Glu Ser Gln Tyr Thr Ile Lys Arg Asp Val Gly Thr Thr
 44 20 25 30
 47 Thr Ala Val Thr Pro Ser Ser Leu Gln Gln Glu Ile Thr Leu Leu Cys
 48 35 40 45
 51 Gly Glu Ile Leu Tyr Ala Lys His Ala Asp Tyr Lys Tyr Ala Ala Glu
 52 50 55 60
 55 Ile Gly Ile Gln Tyr Ile Ser Thr Ala Leu Gly Ser Glu Arg Val Gln
 56 65 70 75 80
 59 Gln Ile Leu Arg Asn Ser Gly Ser Glu Val Gln Val Val Leu Thr Arg
 60 85 90 95
 63 Thr Tyr Ser Leu Gly Lys Ile Lys Asn Asn Lys Gly Glu Asp Leu Gln
 64 100 105 110
 67 Met Leu Asp Ile His Gly Val Glu Lys Ser Trp Val Glu Glu Ile Asp
 68 115 120 125
 71 Lys Glu Ala Arg Lys Thr Met Ala Thr Leu Leu Lys Glu Ser Ser Gly
 72 130 135 140
 75 Asn Ile Pro Gln Asn Gln Arg Pro Ser Ala Pro Asp Thr Pro Ile Ile

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76 145          150          155          160
79 Leu Leu Cys Val Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Ile
80          165          170          175
83 Glu Val Gly Leu Glu Thr Thr Val Arg Arg Ala Asn Arg Val Leu Ser
84          180          185          190
87 Asp Ala Leu Lys Arg Tyr Pro Arg Met Asp Ile Pro Lys Ile Ala Arg
88          195          200          205
91 Ser Phe Tyr Asp Leu Phe Glu Gln Lys Val Tyr His Arg Ser Leu Phe
92          210          215          220
95 Ile Glu Tyr Gly Lys Ala Leu Gly Ser Ser Ser Thr Gly Ser Lys Ala
96 225          230          235          240
99 Glu Ser Leu Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln
100          245          250          255
103 Thr Met Leu Arg Trp Gly Val Ile Ala Arg Ser Ser Asn Asn Ile Met
104          260          265          270
107 Leu Gly His Val Ser Val Gln Ala Glu Leu Lys Gln Val Thr Glu Val
108          275          280          285
111 Tyr Asp Leu Val Arg Glu Met Gly Pro Glu Ser Gly Leu Leu His Leu
112          290          295          300
115 Arg Gln Ser Pro Lys Ala Gly Leu Leu Ser Leu Ala Asn Cys Pro Asn
116 305          310          315          320
119 Phe Ala Ser Val Val Leu Gly Asn Ala Ser Gly Leu Gly Ile Ile Gly
120          325          330          335
123 Met Tyr Arg Gly Arg Val Pro Asn Thr Glu Leu Phe Ser Ala Ala Glu
124          340          345          350
127 Ser Tyr Ala Lys Ser Leu Lys Glu Ser Asn Lys Ile Asn Phe Ser Ser
128          355          360          365
131 Leu Gly Leu Thr Asp Glu Glu Lys Glu Ala Ala Glu His Phe Leu Asn
132          370          375          380
135 Val Ser Asp Asp Ser Gln Asn Asp Tyr Glu
136 385          390
139 <210> SEQ ID NO: 2
140 <211> LENGTH: 391
141 <212> TYPE: PRT
142 <213> ORGANISM: Avian pneumovirus A
144 <400> SEQUENCE: 2
146 Met Ser Leu Glu Ser Ile Arg Leu Ser Asp Leu Glu Tyr Lys His Ala
147 1          5          10          15
150 Ile Leu Glu Asp Ser Gln Tyr Thr Ile Arg Arg Asp Val Gly Ala Thr
151          20          25          30
154 Thr Ala Ile Thr Pro Ser Glu Leu Gln Pro Gln Val Ser Thr Leu Cys
155          35          40          45
158 Gly Met Val Leu Phe Ala Lys His Thr Asp Tyr Glu Pro Ala Ala Glu
159          50          55          60
162 Val Gly Met Gln Tyr Ile Ser Thr Ala Leu Gly Ala Asp Arg Thr Gln
163 65          70          75          80
166 Gln Ile Leu Lys Asn Ser Gly Ser Glu Val Gln Gly Val Met Thr Lys
167          85          90          95
170 Ile Val Thr Leu Ser Ala Glu Gly Ser Val Arg Lys Arg Glu Val Leu

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171          100          105          110
174 Asn Ile His Asp Val Gly Val Gly Trp Ala Asp Asp Val Glu Arg Thr
175          115          120          125
178 Thr Arg Glu Ala Met Gly Ala Met Val Arg Glu Lys Val Gln Leu Thr
179          130          135          140
182 Lys Asn Gln Lys Pro Ser Ala Leu Asp Ala Pro Val Ile Leu Leu Cys
183 145          150          155          160
186 Ile Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Val Glu Val Gly
187          165          170          175
190 Leu Glu Thr Ala Ile Arg Arg Ala Ser Arg Val Leu Ser Asp Ala Ile
191          180          185          190
194 Ser Arg Tyr Pro Arg Met Asp Ile Pro Arg Ile Ala Lys Ser Phe Phe
195          195          200          205
198 Glu Leu Phe Glu Lys Lys Val Tyr Tyr Arg Asn Leu Phe Ile Glu Tyr
199          210          215          220
202 Gly Lys Ala Leu Gly Ser Thr Ser Thr Gly Ser Arg Met Glu Ser Leu
203 225          230          235          240
206 Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln Thr Met Leu
207          245          250          255
210 Arg Trp Gly Val Ile Ala Arg Ser Ser Asn Asn Ile Met Leu Gly His
211          260          265          270
214 Val Ser Val Gln Ala Glu Leu Arg Gln Val Ser Glu Val Tyr Asp Leu
215          275          280          285
218 Val Arg Lys Met Gly Pro Glu Ser Gly Leu Leu His Leu Arg Gln Ser
219          290          295          300
222 Pro Lys Ala Gly Leu Leu Ser Leu Thr Asn Cys Pro Asn Phe Ala Ser
223 305          310          315          320
226 Val Val Leu Gly Asn Ala Ala Gly Leu Gly Ile Ile Gly Met Tyr Lys
227          325          330          335
230 Gly Arg Ala Pro Asn Leu Glu Leu Phe Ala Ala Ala Glu Ser Tyr Ala
231          340          345          350
234 Arg Thr Leu Arg Glu Asn Asn Lys Ile Asn Leu Ala Ala Leu Gly Leu
235          355          360          365
238 Thr Asp Asp Glu Arg Glu Ala Ala Thr Ser Tyr Leu Gly Gly Asp Asp
239          370          375          380
242 Glu Arg Ser Ser Lys Phe Glu
243 385          390
246 <210> SEQ ID NO: 3
247 <211> LENGTH: 391
248 <212> TYPE: PRT
249 <213> ORGANISM: Avian pneumovirus B
251 <400> SEQUENCE: 3
253 Met Ser Leu Glu Ser Ile Arg Leu Ser Asp Leu Glu Tyr Lys His Ala
254 1          5          10          15
257 Ile Leu Asp Glu Ser Gln Tyr Thr Ile Arg Arg Asp Val Gly Ala Thr
258          20          25          30
261 Thr Ala Ile Thr Pro Ser Glu Leu Gln Pro Lys Val Ser Thr Leu Cys
262          35          40          45
265 Gly Met Ile Leu Phe Ala Lys His Ala Asp Tyr Glu Pro Ala Ala Gln

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```

266      50      55      60
269 Val Gly Met Gln Tyr Ile Ser Thr Ala Leu Gly Ala Asp Lys Thr Gln
270 65      70      75      80
273 Gln Ile Leu Lys Ser Ser Gly Ser Glu Val Gln Gly Val Met Thr Lys
274      85      90      95
277 Ile Val Thr Leu Pro Ala Glu Gly Pro Ile Arg Lys Arg Glu Val Leu
278      100      105      110
281 Asn Ile His Asp Ile Gly Pro Ala Trp Ala Asp Asn Val Glu Arg Thr
282      115      120      125
285 Ala Arg Glu Thr Met Ser Leu Met Val Lys Glu Lys Ala Gln Ile Pro
286      130      135      140
289 Lys Asn Gln Lys Pro Ser Ala Leu Asp Ala Pro Val Ile Leu Leu Cys
290 145      150      155      160
293 Ile Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Val Glu Val Gly
294      165      170      175
297 Leu Glu Thr Ala Ile Arg Arg Ala Ser Arg Val Leu Ser Asp Ala Ile
298      180      185      190
301 Ser Arg Tyr Pro Arg Met Asp Ile Pro Arg Ile Ala Lys Ser Phe Phe
302      195      200      205
305 Glu Leu Phe Glu Lys Lys Val Tyr Tyr Arg Asn Leu Phe Ile Glu Tyr
306      210      215      220
309 Gly Lys Ala Leu Gly Ser Thr Ser Ser Gly Ser Arg Met Glu Ser Leu
310 225      230      235      240
313 Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln Thr Met Leu
314      245      250      255
317 Arg Arg Gly Val Val Ala Arg Ser Ser Asn Asn Ile Met Leu Gly His
318      260      265      270
321 Val Ser Val Gln Ala Glu Leu Arg Gln Val Ser Glu Val Tyr Asp Leu
322      275      280      285
325 Val Arg Lys Met Gly Pro Glu Ser Gly Leu Leu His Leu Arg Gln Ser
326      290      295      300
329 Pro Lys Ala Gly Leu Leu Ser Leu Thr Ser Cys Pro Asn Phe Ala Ser
330 305      310      315      320
333 Val Val Leu Gly Asn Ala Ala Gly Leu Gly Ile Ile Gly Met Tyr Lys
334      325      330      335
337 Gly Arg Ala Pro Asn Leu Glu Leu Phe Ser Ala Ala Glu Ser Tyr Ala
338      340      345      350
341 Arg Ser Leu Lys Glu Ser Asn Lys Ile Asn Leu Ala Ala Leu Gly Leu
342      355      360      365
345 Thr Glu Asp Glu Arg Glu Ala Ala Thr Ser Tyr Leu Gly Gly Asp Glu
346      370      375      380
349 Asp Lys Ser Gln Lys Phe Glu
350 385      390
353 <210> SEQ ID NO: 4
354 <211> LENGTH: 394
355 <212> TYPE: PRT
356 <213> ORGANISM: Avian pneumovirus C
358 <400> SEQUENCE: 4
360 Met Ser Leu Gln Gly Ile Gln Leu Ser Asp Leu Ser Tyr Lys His Ala

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```

361 1          5          10          15
364 Ile Leu Lys Glu Ser Gln Tyr Thr Ile Lys Arg Asp Val Gly Thr Thr
365          20          25          30
368 Thr Ala Val Thr Pro Ser Ser Leu Gln Arg Glu Val Ser Leu Leu Cys
369          35          40          45
372 Gly Glu Ile Leu Tyr Ala Lys His Thr Asp Tyr Ser His Ala Ala Glu
373          50          55          60
376 Val Gly Met Gln Tyr Val Ser Thr Thr Leu Gly Ala Glu Arg Thr Gln
377 65          70          75          80
380 Gln Ile Leu Lys Asn Ser Gly Ser Glu Val Gln Ala Val Leu Thr Lys
381          85          90          95
384 Thr Tyr Ser Leu Gly Lys Gly Lys Asn Ser Lys Gly Glu Glu Leu Gln
385          100          105          110
388 Met Leu Asp Ile His Gly Val Glu Arg Ser Trp Ile Glu Glu Val Asp
389          115          120          125
392 Lys Glu Ala Arg Lys Thr Met Ala Ser Ala Thr Lys Asp Asn Ser Gly
393          130          135          140
396 Pro Ile Pro Gln Asn Gln Arg Pro Ser Ser Pro Asp Ala Pro Ile Ile
397 145          150          155          160
400 Leu Leu Cys Ile Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Ile
401          165          170          175
404 Glu Val Gly Leu Glu Thr Ala Val Arg Arg Ala Asn Arg Val Leu Asn
405          180          185          190
408 Asp Ala Leu Lys Arg Phe Pro Arg Ile Asp Ile Pro Lys Ile Ala Arg
409          195          200          205
412 Ser Phe Tyr Asp Leu Phe Glu Gln Lys Val Tyr Tyr Arg Ser Leu Phe
413          210          215          220
416 Ile Glu Tyr Gly Lys Ala Leu Gly Ser Ser Ser Thr Gly Ser Lys Ala
417 225          230          235          240
420 Glu Ser Leu Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln
421          245          250          255
424 Thr Met Leu Arg Trp Gly Val Ile Ala Arg Ser Ser Asn Asn Ile Met
425          260          265          270
428 Leu Gly His Val Ser Val Gln Ala Glu Leu Lys Gln Val Thr Glu Val
429          275          280          285
432 Tyr Asp Leu Val Arg Glu Met Gly Pro Glu Ser Gly Leu Leu His Leu
433          290          295          300
436 Arg Gln Asn Pro Lys Ala Gly Leu Leu Ser Leu Ala Asn Cys Pro Asn
437 305          310          315          320
440 Phe Ala Ser Val Val Leu Gly Asn Ala Ser Gly Leu Gly Ile Leu Gly
441          325          330          335
444 Met Tyr Arg Gly Arg Val Pro Asn Thr Glu Leu Phe Ala Ala Ala Glu
445          340          345          350
448 Ser Tyr Ala Arg Ser Leu Lys Glu Ser Asn Lys Ile Asn Phe Ser Ser
449          355          360          365
452 Leu Gly Leu Thr Glu Glu Glu Lys Glu Ala Ala Glu Asn Phe Leu Asn
453          370          375          380
456 Ile Asn Glu Glu Gly Gln Asn Asp Tyr Glu
457 385          390

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/722,045

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:105; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:105; Xaa Pos. 29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47
Seq#:105; Xaa Pos. 48
Seq#:106; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:106; Xaa Pos. 23,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47
Seq#:106; Xaa Pos. 48
Seq#:133; N Pos. 6
Seq#:135; N Pos. 6,9
Seq#:138; N Pos. 4
Seq#:142; N Pos. 10,19
Seq#:143; N Pos. 17

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:101,102,103,104,107,108,109,110,111,112,113,114,115,116,117,118,119,120
Seq#:121,122,123,124,125,126,127,128,129,130,131,132,133,134,135,136,137,138
Seq#:139,140,141,142,143,144,145,146,147,148,149,150,151,152,153,154,155,156
Seq#:157,158,159,160,161,162,163,164,165

VERIFICATION SUMMARY

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L:6726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:105 after pos.:0
M:341 Repeated in SeqNo=105
L:6760 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106 after pos.:0
M:341 Repeated in SeqNo=106
L:7103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:133 after pos.:0
L:7138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135 after pos.:0
L:7180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:138 after pos.:0
L:7239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:142 after pos.:0
L:7257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:143 after pos.:0